IN THE SPECIFICATIONS:

Please **amend** the specifications as follows (amendments are underlined):

The paragraph bridging pages 5–6 of the instant specification:

Computer-assisted analysis suggests that mature IL-17RLM-L contains a putative signal peptide of 16 amino acids, a 281-amino acid extracellular domain (C17-Pro297), a 23-amino acid transmembrane stretch (Ile298-Met320), and a 420-amino acid longer cytoplasmic tail (Cys321-Leu739) than that of IL-17BR/IL-17Rh1. The cytoplasmic portion of this new receptor polypeptide of the invention is much longer than IL-17BR, and is comparable with the unusually long tail described for IL-17 receptor. Additionally, there are nine cystine residues in extracellular domain and eight potential N-linked glycosylation sites in the extracellular domain of the polypeptide of the invention. The extracellular domain also consists of a predicted immunoglobulin domain and a putative fibronectin III domain. This protein is predicted to be a type I membrane protein according to Hartmann membrane topology model and PSORT II server prediction. But there is no WSXWS (SEQ ID NO:20) motif, typical of type I receptor (32,33) in the extracellular domain. The sequence of IL-17RLM-L is slightly atypical for type I cytokine receptors in that the usual WSXWS (SEQ ID NO:20) motif is replaced by WSPGA (SEQ ID NO:21). Furthermore, a segment (TPPPLRPRKVW (SEQ ID NO:22)) located proximal to the IL-17 receptor transmembrane domain, which is highly conserved among cytokine receptor, is replaced by the proline-rich motif (PFHPPPLRYREP (SEQ ID NO:23)), which was a typical feature of a transactivation domain for transcription factors. Interestingly, both a putative TIR domain (Toll/IL-1-Receptor homology domain) and a putative SH3 interaction domain (proline-rich domain) were predicted in the intracellular domain of the protein from (V358 to K424). Additionally, a putative tyrosine phosphorylation site juxtapsed to the transmembrane domain (Y329) was also identified. The long COOH-terminal tail (C-tail) of IL-17RLM also contains multiple tyrosine residues and putative Stat binding motifs.

At page 10, 3rd paragraph of the instant specification:

Electrophoretic mobility-shift assay DNA probes [double-stranded β-casein promoter GAS (γ-interferon activated sequence): 5'-AGATTTCTAGGAATTC-3' (SEQ ID NO:19)] were prepared by end-labeling with [γ-^{32}P]ATP and T4 polynucleotide kinase and purified by G-50 MicroSpin columns. Cells were washed three times in PBS and starved in the absence of cytokines for 8 hrs in RPMI 1640. Cells were then stimulated for the indicated times with the indicated cytokine at a concentration used in growth medium. Typically, 5μl (10-20μg) of nuclear proteins was incubated with 100,000 cpm of ^{32}P-labeled oligonucleotides for 2 hrs at room temperature. The nuclear proteins and various oligonucleotide probes were incubated in buffer containing 10 mM Tris (pH 7.5), 10% glycerol, and 0.2% Nonidet P-40. Additionally, 2-4μg of poly (dI-dC) was included as a nonspecific competitor DNA. Protein-DNA complexes were resolved on 4% nondenaturing polyacrylamide gels in 0.5×TBE running buffer. After electrophoresis, gels were dried and subjected to autoradiography. Antibody supershift experiments were carried out by addition of 4μl of various antibodies purchased from Santa Cruz Biotechnology.

At page 13, 1st paragraph of the instant specification:

Computer-assisted analysis suggested that hIL-17RLM-L contained a putative signal peptide of 16 amino acids, a 281-amino acid extracellular domain (C^{17}-Pro^{297}), a 23-amino acid transmembrane stretch (Ile^{298}-Met^{320}), and a 420-amino acid cytoplasmic tail (Cys^{321}-Leu^{739}). The cytoplasmic portion of this new receptor was much longer than that of IL-17BR, and comparable with the unusually long tail of IL-17AR. This protein was predicted to be a type I cytokine receptor according to Hartmann membrane topology model and PSORT II server. However, hIL-17RLM-L had a WSPGA (SEQ ID NO:21) instead of WSXWS (SEQ ID NO:20) motif, which is a typical motif in the extracellular domain of type I cytokine receptors (33, 34). There were eight cystine residues and nine potential N-linked glycosylation sites in the extracellular domain, where an immunoglobulin domain and a fibronectin III domain were also predicted. Furthermore, a highly cytokine receptor conserved segment (TPPPLRPRKVW (SEQ ID NO:22)) located proximal to the IL-17

receptor transmembrane domain was replaced by the proline-rich segment (PFHPPPLRYREP (SEQ ID NO:23)), a putative SH3 interaction domain, which was a typical feature of a transactivation domain for transcription factors. Additionally, a putative TIR domain (V^{358} to K^{424}) (Toll/IL-1Receptor domain) and a putative TRAF6 binding motif (P^{347} to L^{351}), Pro-X-Glu-X-X (aromatic/acidic residue) were predicted in the intracellular portion of hIL-17RLM-L. The TRAF6 binding motif was found in TRANCE-R and IRAK adapter kinases for ILR/Toll-like receptor signaling(35), suggesting that hIL-17RLM may play a role in the Toll-like receptor signaling. The long COOH-terminal tail (C-tail) of hIL-17RLM also contained multiple tyrosine residues. All of these implied that the protein might be a novel signaling receptor.

Please **delete** the prior "SEQUENCE LISTING" and **replace** it with the following revised SEQUENCE LISTING (changes relative to the previous version are underlined):

SEQUENCE LISTING

<110> Tsinghua University

<120> Human Interleukin-17 Receptor Like Molecule

<130> I2003269C-US

<160> 23

<170> PatentIn version 3.1

<210> 1
<211> 4477
<212> DNA
<213> Homo sapiens

<400> 1
gcggccgccg cggccaccgc ccactcgggg ctggccagcg gcgggcggcc ggggcgcaga
60

gaacggcctg gctgggcgag cgcacggcca tggccccgtg gctgcagctc tgctccgtct
120

tctttacggt caacgcctgc ctcaacggct cgcagctggc tgtggccgct ggcgggtccg
180

gccgcgcgcg gggcgccgac acctgtggct ggaggggagt ggggccagcc agcagaaaca
240

gtgggctgta caacatcacc ttcaaatatg acaattgtac cacctacttg aatccagtgg
300

ggaagcatgt gattgctgac gcccagaata tcaccatcag ccagtatgct tgccatgacc
360

aagtggcagt caccattctt tggtccccag gggccctcgg catcgaattc ctgaaaggat
420

ttcgggtaat actggaggag ctgaagtcgg agggaagaca gtgccaacaa ctgattctaa
480

aggatccgaa gcagctcaac agtagcttca aaagaactgg aatggaatct caacctttcc
540

tgaatatgaa atttgaaacg gattatttcg taaaggttgt ccctttтcct tccattaaaa
600

acgaaagcaa ttaccaccct ttcttcttta gaacccgagc ctgtgacctg ttgttacagc
660

cggacaatct agcttgtaaa cccttctgga agcctcggaa cctgaacatc agccagcatg
720

gctcggacat gcaggtgtcc ttcgaccacg caccgcacaa cttcggcttc cgtttcttct
780

atcttcacta caagctcaag cacgaaggac ctttcaagcg aaagacctgt gagcaggagc
840

aaactacaga gatgaccagc tgcctccttc aaaatgtttc tccaggggat tatataattg
900

agctggtgga tgacactaac acaacaagaa aagtgatgca ttatgcctta aagccagtgc
960

actccccgtg ggccgggccc atcagagccg tggccatcac agtgccactg gtagtcatat
1020

cggcattcgc gacgctcttc actgtgatgt gccgcaagaa gcaacaagaa aatatatatt
1080

cacatttaga tgaagagagc tctgagtctt ccacatacac tgcagcactc ccaagagaga
1140

ggctccggcc gcggccgaag gtctttctct gctattccag taaagatggc cagaatcaca
1200

tgaatgtcgt ccagtgtttc gcctacttcc tccaggactt ctgtggctgt gaggtggctc
1260

tggacctgtg ggaagacttc agcctctgta gagaagggca gagagaatgg gtcatccaga
1320

agatccacga gtcccagttc atcattgtgg tttgttccaa aggtatgaag tactttgtgg
1380

acaagaagaa ctacaaacac aaaggaggtg gccgaggctc ggggaaagga gagctcttcc
1440

tggtggcggt gtcagccatt gccgaaaagc tccgccaggc caagcagagt tcgtccgcgg
1500

cgctcagcaa gtttatcgcc gtctactttg attattcctg cgagggagac gtccccggta
1560

tcctagacct gagtaccaag tacagactca tggacaatct tcctcagctc tgttcccacc
1620

tgcactcccg agaccacggc ctccaggagc cggggcagca cacgcgacag ggcagcagaa
1680

ggaactactt ccggagcaag tcaggccggt ccctatacgt cgccatttgc aacatgcacc
1740

agtttattga cgaggagccc gactggttcg aaaagcagtt cgttcccttc catcctcctc
1800

cactgcgcta ccgggagcca gtcttggaga aatttgattc gggcttggtt ttaaatgatg
1860

tcatgtgcaa accagggcct gagagtgact tctgcctaaa ggtagaggcg gctgttcttg
1920

gggcaaccgg accagccgac tcccagcacg agagtcagca tgggggcctg gaccaagacg
1980

gggaggcccg gcctgccctt gacggtagcg ccgccctgca acccctgctg cacacggtga
2040

aagccggcag cccctcggac atgccgcggg actcaggcat ctatgactcg tctgtgccct
2100

catccgagct gtctctgcca ctgatggaag gactctcgac ggaccagaca gaaacgtctt
2160

ccctgacgga gagcgtgtcc tcctcttcag gcctgggtga ggaggaacct cctgcccttc
2220

cttccaagct cctctcttct gggtcatgca aagcagatct tggttgccgc agctacactg
2280

atgaactcca cgcggtcgcc cctttgtaac aaaacgaaag agtctaagca ttgccacttt
2340

agctgctgcc tccctctgat tccccagctc atctccctgg ttgcatggcc cacttggagc
2400

tgaggtctca tacaaggata tttggagtga aatgctggcc agtacttgtt ctcccttgcc
2460

ccaacccttt accggatatc ttgacaaact ctccaatttt ctaaaatgat atggagctct
2520

gaaaggcatg tccataaggt ctgacaacag cttgccaaat ttggttagtc cttggatcag
2580

agcctgttgt gggaggtagg gaggaaatat gtaaagaaaa acaggaagat acctgcacta
2640

atcattcaga cttcattgag ctctgcaaac tttgcctgtt tgctattggc taccttgatt
2700

tgaaatgctt tgtgaaaaaa ggcactttta acatcatagc cacagaaatc aagtgccagt
2760

ctatctggaa tccatgttgt attgcagata atgttctcat ttatttttga tgtagaattt
2820

acattgccat gggtgttaaa taagctttga gtcaaaagtc aagaaagtga ctgaatatac
2880

agtcaccttt tatgaaatga gtctctgtgt tactgggtgg catgactgat tgaggtgaag
2940

ctcacggggc caggctgacc gtcttgaccg ttccacttga gataggttgg tcatcgtgca
3000

gaaggcccca ggacctcagc acacacagcc tcctcttggt ctgagtaggc atcatgtggg
3060

ggccagatct gcctgctgtt tccatgggtt acatttactg tgctgtatct cagatgttgg
3120

tgtctggaag tttattctta agagactgct acccagctgg tctgtattat tggaagttgc
3180

agttcgtgct ttggttggcc ttctggtcta aagctgtgtc ctgaatatta gggatcacaa
3240

ttcactgaaa tacagcagtg tgtggaggtg atggccagtt aatctgctga actggttttg
3300

actaatgaca aacctctttt taagatggta gaatggaggt gatagtcaca aaagtaaatg
3360

ttccattttt atgaatgact ttctacagag tttctatttc taaagaaaaa acaattgttc
3420

acatcccatc tgatgattag catgtgtgta atgaatgctg tcttggtctc ccctgtggaa
3480

acccttctcc ctgtgcctta gagcaggtgt gtacatctct cactaccttt ctcatgggtg
3540

ctgttagatt ttggcacccg ttttctcagc attcagccca gggaatgtgg ttttcacttc
3600

ttcgtcagat aagaccaaca tgaaggggta tgttgagaaa catcctgagg caaggtggga
3660

ggtgggatgg ggcaggactt tcccttccaa gcacatgcat ggcaggtggg gaaaggggg
3720

cttgcacccc tgctggaaag aaaaggtttg tgtatatttc tgatgcaaat gtcatactca
3780

ctgctctgta aaggcagctg gcagcttttt gggaaaagaa cgtgctcgtc tgttctctgg
3840

catcaagttt cttgcagctg ctctgaggga gagacagtga gctgcaagac tgcctcccca
3900

taacaacagg caactcagag aagagtcatt ttatgttgtt cctatggaat ctggaatgag
3960

tgcagagctc ctacccacac atgactgccc cgccatttca tcctaggcat tctgtgaagg
4020

agattggtta gtccaaactt gctaacatac gaaaattcac ttggaacatg atgagagatt
4080

tcttattgag gccaagagat gtttcctgtc ccagaggaac cattaggagt cgcttttagg
4140

gtattcagct ttgttcatga ataaggcat ctctgagaaa gtggccccag ggagagaatg
4200

gaggactggg aggagaagca ttaactgagc tccaagggtg tgtgggcaga gagcttgcta
4260

tgtgaactca ctccttaaga aaatggaaga gaaaaagaga gtgctagtta aaaaatcggg
4320

atgttttagt ttggatttag ggttttgata cttatgttga aatactaatg tttctgatca
4380

ataaaatcaa actcttaata taccgagtaa tgaaaccata gtgtgattgc ctcagaataa
4440

attgagaagt ccaaaaaaaa aaaaaaaaaa aaaaaaa
4477

<210> 2
<211> 739
<212> PRT
<213> Homo sapiens

<400> 2

Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val Asn Ala
1 5 10 15

Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg
20 25 30

Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Gly Val Gly Pro Ala Ser
35 40 45

Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr
50 55 60

Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn
65 70 75 80

Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile
85 90 95

Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg
100 105 110

Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu
115 120 125

Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly
130 135 140

Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe
145 150 155 160

Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His
165 170 175

Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp
180 185 190

Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser
195 200 205

```
Gln His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn
    210                 215                 220

Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly
225                 230                 235                 240

Pro Phe Lys Arg Lys Thr Cys Glu Gln Glu Gln Thr Thr Glu Met Thr
                245                 250                 255

Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu
            260                 265                 270

Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys
        275                 280                 285

Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr
    290                 295                 300

Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met
305                 310                 315                 320

Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu
                325                 330                 335

Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu
            340                 345                 350

Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln
        355                 360                 365

Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe
    370                 375                 380
```

Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys
385 390 395 400

Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln
405 410 415

Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys
420 425 430

Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu
435 440 445

Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala
450 455 460

Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe
465 470 475 480

Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr
485 490 495

Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His
500 505 510

Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly
515 520 525

Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val
530 535 540

Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe
545 550 555 560

Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu
565 570 575

Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met
580 585 590

Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala
595 600 605

Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His
610 615 620

Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser
625 630 635 640

Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser
645 650 655

Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser
660 665 670

Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu
675 680 685

Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu
690 695 700

Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys
705 710 715 720

Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val
725 730 735

Ala Pro Leu

<210> 3
<211> 4508
<212> DNA
<213> Homo sapiens

<400> 3
cagcagtggt aacgacgcac agtacgcggg ggaaaagaaa cgggaagtgg ccgtgggccg
60

gtgaattccg tgtagtggcc aagctttgtt ccaaagaggg ggaggtggtg acagtctctt
120

gcccactgaa gcgtgccaga cagagtgcta ggcatggggg cagaggtgaa tcagatgaca
180

gccacctctc accacgagga gtggctgaaa gtgtgactgg actacaggca atcctggcct
240

tggcagggag tggggccagc cagcagaaac agtgggctgt acaacatcac cttcaaatat
300

gacaattgta ccacctactt gaatccagtg gggaagcatg tgattgctga cgcccagaat
360

atcaccatca gccagtatgc ttgccatgac caagtggcag tcaccattct ttggtcccca
420

ggggccctcg gcatcgaatt cctgaaagga tttcgggtaa tactggagga gctgaagtcg
480

gagggaagac agtgccaaca actgattcta aaggatccga agcagctcaa cagtagcttc
540

aaaagaactg gaatggaatc tcaacctttc ctgaatatga aatttgaaac ggattatttc
600

gtaaaggttg tccctttttcc ttccattaaa aacgaaagca attaccaccc tttcttcttt
660

agaacccgag cctgtgacct gttgttacag ccggacaatc tagcttgtaa acccttctgg
720

aagcctcgga acctgaacat cagccagcat ggctcggaca tgcaggtgtc cttcgaccac
780

gcaccgcaca acttcggctt ccgtttcttc tatcttcact acaagctcaa gcacgaagga
840

cctttcaagc gaaagacctg taagcaggag caaactacag agatgaccag ctgcctcctt
900

caaaatgttt ctccagggga ttatataatt gagctggtgg atgacactaa cacaacaaga
960

aaagtgatgc attatgcctt aaagccagtg cactccccgt gggccgggcc catcagagcc
1020

gtggccatca cagtgccact ggtagtcata tcggcattcg cgacgctctt cactgtgatg
1080

tgccgcaaga agcaacaaga aaatatatat tcacatttag atgaagagag ctctgagtct
1140

tccacataca ctgcagcact cccaagagag aggctccggc cgcggccgaa ggtctttctc
1200

tgctattcca gtaaagatgg ccagaatcac atgaatgtcg tccagtgttt cgcctacttc
1260

ctccaggact tctgtggctg tgaggtggct ctggacctgt gggaagactt cagcctctgt
1320

agagaagggc agagagaatg ggtcatccag aagatccacg agtcccagtt catcattgtg
1380

gtttgttcca aaggtatgaa gtactttgtg gacaagaaga actacaaaca caaaggaggt
1440

ggccgaggct cggggaaagg agagctcttc ctggtggcgg tgtcagccat tgccgaaaag
1500

ctccgccagg ccaagcagag ttcgtccgcg gcgctcagca agtttatcgc cgtctacttt
1560

gattattcct gcgagggaga cgtccccggt atcctagacc tgagtaccaa gtacagactc
1620

atggacaatc ttcctcagct ctgttcccac ctgcactccc gagaccacgg cctccaggag
1680

ccggggcagc acacgcgaca gggcagcaga aggaactact tccggagcaa gtcaggccgg
1740

tccctatacg tcgccatttg caacatgcac cagtttattg acgaggagcc cgactggttc
1800

gaaaagcagt tcgttccctt ccatcctcct ccactgcgct accgggagcc agtcttggag
1860

aaatttgatt cgggcttggt tttaaatgat gtcatgtgca aaccagggcc tgagagtgac
1920

ttctgcctaa aggtagaggc ggctgttctt ggggcaaccg gaccagccga ctcccagcac
1980

gagagtcagc atgggggcct ggaccaagac ggggaggccc ggcctgccct tgacggtagc
2040

gccgccctgc aacccctgct gcacacggtg aaagccggca gcccctcgga catgccgcgg
2100

gactcaggca tctatgactc gtctgtgccc tcatccgagc tgtctctgcc actgatggaa
2160

ggactctcga cggaccagac agaaacgtct tccctgacgg agagcgtgtc ctcctcttca
2220

ggcctgggtg aggaggaacc tcctgccctt ccttccaagc tcctctcttc tgggtcatgc
2280

aaagcagatc ttggttgccg cagctacact gatgaactcc acgcggtcgc ccctttgtaa
2340

caaaacgaaa gagtctaagc attgccactt tagctgctgc ctccctctga ttccccagct
2400

catctccctg gttgcatggc ccacttggag ctgaggtctc atacaaggat atttggagtg
2460

aaatgctggc cagtacttgt tctcccttgc cccaaccctt taccggatat cttgacaaac
2520

tctccaattt tctaaaatga tatggagctc tgaaaggcat gtccataagg tctgacaaca
2580

gcttgccaaa tttggttagt ccttggatca gagcctgttg tgggaggtag ggaggaaata
2640

tgtaaagaaa aacaggaaga tacctgcact aatcattcag acttcattga gctctgcaaa
2700

ctttgcctgt ttgctattgg ctaccttgat ttgaaatgct ttgtgaaaaa aggcactttt
2760

aacatcatag ccacagaaat caagtgccag tctatctgga atccatgttg tattgcagat
2820

aatgttctca tttatttttg atgtagaatt tacattgcca tgggtgttaa ataagctttg
2880

agtcaaaagt caagaaagtg actgaatata cagtcacctt ttatgaaatg agtctctgtg
2940

ttactgggtg gcatgactga ttgaggtgaa gctcacgggg ccaggctgac cgtcttgacc
3000

gttccacttg agataggttg gtcatcgtgc agaaggcccc aggacctcag cacacacagc
3060

ctcctcttgg tctgagtagg catcatgtgg gggccagatc tgcctgctgt ttccatgggt
3120

tacatttact gtgctgtatc tcagatgttg gtgtctggaa gtttattctt aagagactgc
3180

tacccagctg gtctgtatta ttggaagttg cagttcgtgc tttggttggc cttctggtct
3240

aaagctgtgt cctgaatatt agggatcaca attcactgaa atacagcagt gtgtggaggt
3300

gatggccagt taatctgctg aactggtttt gactaatgac aaacctcttt ttaagatggt
3360

agaatggagg tgatagtcac aaaagtaaat gttccatttt tatgaatgac tttctacaga
3420

gtttctattt ctaaagaaaa aacaattgtt cacatcccat ctgatgatta gcatgtgtgt
3480

aatgaatgct gtcttggtct cccctgtgga aacccttctc cctgtgcctt agagcaggtg
3540

tgtacatctc tcactacctt tctcatgggt gctgttagat tttggcaccc gttttctcag
3600

cattcagccc agggaatgtg gttttcactt cttcgtcaga taagaccaac atgaaggggt
3660

atgttgagaa acatcctgag gcaaggtggg aggtgggatg gggcaggact ttcccttcca
3720

agcacatgca tggcaggtgg ggaaaggggg gcttgcaccc ctgctggaaa gaaaaggttt
3780

gtgtatattt ctgatgcaaa tgtcatactc actgctctgt aaaggcagct ggcagctttt
3840

tgggaaaaga acgtgctcgt ctgttctctg gcatcaagtt tcttgcagct gctctgaggg
3900

agagacagtg agctgcaaga ctgcctcccc ataacaacag gcaactcaga gaagagtcat
3960

tttatgttgt tcctatggaa tctggaatga gtgcagagct cctacccaca catgactgcc
4020

ccgccatttc atcctaggca ttctgtgaag gagattggtt agtccaaact tgctaacata
4080

cgaaaattca cttggaacat gatgagagat ttcttattga ggccaagaga tgtttcctgt
4140

cccagaggaa ccattaggag tcgcttttag ggtattcagc tttgttcatg aaataaggca
4200

tctctgagaa agtggcccca gggagagaat ggaggactgg gaggagaagc attaactgag
4260

ctccaagggt gtgtgggcag agagcttgct atgtgaactc actccttaag aaaatggaag
4320

agaaaaagag agtgctagtt aaaaaatcgg gatgttttag tttggattta gggttttgat
4380

acttatgttg aaatactaat gtttctgatc aataaaatca aactcttaat ataccgagta
4440

atgaaaccat agtgtgattg cctcagaata aattgagaag tccaaaaaaa aaaaaaaaaa
4500

aaaaaaaa
4508

<210> 4
<211> 595
<212> PRT
<213> Homo sapiens

<400> 4

Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe
1 5 10 15

Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His
20 25 30

Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp
35 40 45

Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser
50 55 60

Gln His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn
65 70 75 80

Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly
85 90 95

Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met Thr
100 105 110

Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu
115 120 125

Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys
130 135 140

Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr
145 150 155 160

Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met
165 170 175

Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu
180 185 190

Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu
195 200 205

Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln
210 215 220

Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe
225 230 235 240

Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys
245 250 255

Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln
260 265 270

Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys
275 280 285

Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu
290 295 300

Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala
305 310 315 320

Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe
325 330 335

Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr
340 345 350

Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His
355 360 365

Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly
370 375 380

Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val
385 390 395 400

Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe
405 410 415

Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu
420 425 430

Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met
435 440 445

Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala
450 455 460

Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His
465 470 475 480

Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser
485 490 495

Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser
500 505 510

Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser
515 520 525

Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu
530 535 540

Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu
545 550 555 560

Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys
565 570 575

Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val
580 585 590

Ala Pro Leu
595

<210> 5
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 5
tatagcgata tcatggacaa actcagggtg cc
32

<210> 6
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 6
aatgaattcc taggagcagg ccacatagcc
30

<210> 7
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 7
ataaagctta tggccccgtg gctgc
25

<210> 8
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 8
ttctcgagtt acaaaggggc gaccgc
26

<210> 9
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 9
tatagcgata tcatggacaa actcagggtg cc
32

<210> 10
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 10
tatagaattc cagcagggcc agaaccgtc
29

<210> 11
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 11
attgaattct gccgcaagaa gcaac
25

<210> 12
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 12
attggatcct tacaaagggg cgaccgc
27

<210> 13
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 13
ataggtacca tggaatctca acctttcctg
30

<210> 14
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 14

ataggatccc aaaggggcga ccgcg
25

<210> 15
<211> 31
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 15
cgtggtaccg atggaatctc aacctttcct g
31

<210> 16
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 16
atatctagag ggcccggccc acgg
24

<210> 17
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 17
agctcaccat ggatgatgat atc
23

<210> 18

<211> 24
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 18
tgttgaaggt ctcaaacatg atct
24

<210> 19
<211> 16
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 19
agatttctag gaattc
16

<210> 20
<211> 5
<212> PRT
<213> Homo sapiens

<400> 20

Trp Ser Xaa Trp Ser
1 5

<210> 21
<211> 5
<212> PRT
<213> Homo sapiens

<400> 21

Trp Ser Pro Gly Ala

1 5

<210> 22
<211> 11
<212> PRT
<213> Homo sapiens

<400> 22

Thr Pro Pro Pro Leu Arg Pro Arg Lys Val Trp
1 5 10

<210> 23
<211> 12
<212> PRT
<213> Homo sapiens

<400> 23

Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro
1 5 10